

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2002, 02:09:30 ; Search time 8718.72 Seconds
(without alignments)
2592.199 Million cell updates/sec

Title: US-09-719-748-1_COPY_62_1141

Perfect score: 1080

Sequence: 1 atggagcattcaagcagca.....ggaggaggagcagcactcc 1080

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pi.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description

1	1075.2	99.6	1742	9	AF052941	AF052941 Homo sapi
2	1072	99.3	1739	9	AB018001	AB018001 Homo sapi
3	937.6	86.8	1883	10	BC022165	BC022165 Mus muscu
4	932.8	86.4	1757	10	AB018002	AB018002 Mus muscu
5	778.2	72.1	1474	10	AF052942	AF052942 Mus muscu
6	524.2	48.5	5345	19	MMDAPK	X97048 M.musculus
7	516.2	47.8	2055	9	AB022341	AB022341 Homo sapi
8	514.6	47.6	2105	9	AB007144	AB007144 Homo sapi
9	514.6	47.6	2132	6	AR076189	AR076189 Sequence
10	514.6	47.6	2132	6	AR124102	AR124102 Sequence
11	514.6	47.6	2132	6	E23384	E23384 DNA encodin
12	514.6	47.6	2224	6	BD004888	BD004888 Novel gen
13	514.6	47.6	2224	9	AB027590	AB027590 Homo sapi
14	512.8	47.5	1410	10	AB007143	AB007143 Mus muscu
15	512.8	47.5	1429	6	AR076190	AR076190 Sequence
16	512.8	47.5	1429	6	AR124103	AR124103 Sequence
17	512.8	47.5	1429	6	E23385	E23385 DNA encodin
18	498.4	46.1	1514	10	RN06971	AJ006971 Rattus no
19	495.4	45.9	1590	9	BC003614	BC003614 Homo sapi
20	493.8	45.7	5910	9	HSDAPK	X76104 H.sapiens D
21	448.6	41.5	4935	6	AR080622	AR080622 Sequence
22	448.6	41.5	5886	6	AR121934	AR121934 Sequence
23	445.4	41.2	480	6	AR119795	AR119795 Sequence
24	445.4	41.2	480	6	AR126755	AR126755 Sequence
25	445.4	41.2	480	6	AR128915	AR128915 Sequence
26	445.4	41.2	480	6	AR130846	AR130846 Sequence
27	445.4	41.2	480	6	AR138891	AR138891 Sequence
28	445.4	41.2	480	6	AR141359	AR141359 Sequence
29	445.4	41.2	1864	6	AR119794	AR119794 Sequence
30	445.4	41.2	1864	6	AR126754	AR126754 Sequence
31	445.4	41.2	1864	6	AR128914	AR128914 Sequence
32	445.4	41.2	1864	6	AR130845	AR130845 Sequence
33	445.4	41.2	1864	6	AR138890	AR138890 Sequence
34	445.4	41.2	1864	6	AR141358	AR141358 Sequence
35	359.2	33.3	4918	10	BC021490	BC021490 Mus muscu
36	244.6	22.6	132817	2	AC011488	AC011488 Homo sapi
37	244.6	22.6	210617	2	AC034201	AC034201 Homo sapi
38	239.4	22.2	247196	2	AC073822	AC073822 Mus muscu
39	222.4	20.6	194023	9	AC021541	AC021541 Homo sapi
40	215.8	20.0	3983	4	S57131	S57131 155 kda myo
41	207.8	19.2	2960	9	AB056801	AB056801 Macaca fa
42	205.4	19.0	1366	3	ACTWITCH	Z30161 A.californi
43	205	19.0	1317	4	S80867	S80867 Ovis aries
44	203	18.8	1415	9	HSMTOLCKI	X90870 H.sapiens m
45	203	18.8	3181	9	AB037663	AB037663 Homo sapi

ALIGNMENTS

RESULT	1
AF052941	
LOCUS	AF052941 1742 bp mRNA linear PRI 20-JAN-2000
DEFINITION	Homo sapiens DAP-kinase related protein 1 mRNA, complete cds.
ACCESSION	AF052941
VERSION	AF052941.1 GI:3560542
KEYWORDS	human.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	1 (bases 1 to 1742)
AUTHORS	Inbal,B., Shani,G., Cohen,O., Kissil,J.L. and Kimchi,A.
TITLE	Death-associated protein kinase-related protein 1, a novel Serine/threonine kinase involved in apoptosis
JOURNAL	Mol. Cell. Biol. 20 (3), 1044-1054 (2000)
MEDLINE	20094983
PUBMED	10629061
REFERENCE	2 (bases 1 to 1742)
AUTHORS	Kimchi,A. and Inbal,B.
TITLE	Direct Submission
JOURNAL	Submitted (09-MAR-1998) Molecular Genetics, Weizmann Institute of Science, Rehovot 76100, Israel

FEATURES		Location/Qualifiers
source	1..1742	/organism="Homo sapiens"
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	32..1144	
CDS	/note="protein serine/threonine kinase"	
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	/translation="MFQASMRSPNMEPFKQKVEDFYDIGELSGGQFAIVKKCREKS	
	TGLEVAAKFIKKRQSRASRGVREIEREYSILRQVLHNVITLHDVYENRTDVLIL	
	LELVSGGELFLAQKESLESEATSFQKLDGVNLYHTKKIAHFDLKPENIMLLDK	
	NIPPIHKLIDFLGAHEIDEGVEFNIFGFEVAPELVIVNIEPLGLEADMWSIGVTY	
	ILLSGASPLGDTKQETLANITSYDFDEEFFSHSELAKDFIRKLLKYEKRRLTI	
misc_feature	923..1021	/note="calcium/calmodulin binding region; binding site"
	441 a	437 c 504 g 360 t
	BASE COUNT	
	ORIGIN	
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	Best Local Similarity 99.7%; Pred. No. 4.8e-231;	
	Matches 1077; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	1	atgaagccatcaagcagcagaaggtggaggacttttatgacatcgagagagctgggg 60
DB	62	ATGGAGCCATTCAGACGACGAGGTGGAGACTTTTATGACATCGAGAGAGCTGGG 121
QY	61	agtggccagtttgcctatgtaaaadtcgagagagcgcgggcttgagtgatgca 120
DB	122	AGTGGCCAGTTTGGCATCGTGAAGAAGTGCCTGGGAGAGACGCGGGCTTGAGTATGCA 181
QY	121	gccaatgtcatcaagaagcgcagagcggcgagcgccggcgcggtgtgagcgggagag 180
DB	182	GCCAACTTCATCAAGAAGCGGACAGCGCGGCGGCGCGGCGGTGTGAGCCGGAGGAG 241
QY	181	atcagcgggaggtgagcattcctgcgcagagtgctgcaccacaatgtcatcaogctgac 240
DB	242	ATCGAGCGGAGGTGAGCATCTCTGGCAGGTGCTGCACCAATGTCTATCACCTGCAC 301
QY	241	gagctctatgagacccgacacgtgggtgcacatccttgagctagctgtcggaggagag 300
DB	302	GACGTCTATGAGAACCGCACCGACGCTGTCTCTCTTGTAGCTAGTGTCTGGAGGAG 361
QY	301	ctctcgattctctggccagagaggtcactgagtgagggaggagccaccagcttcatt 360
DB	362	CTCTTCGATTTCCTTGGCCCAAGAGGAGTCACTGAGTGAGGAGGCGCCACCACTTCAT 421
QY	361	aagcagatcctggatgggtgaaactaccttcacacaaaagaaatgctcactttgatctc 420
DB	422	AAGCAGATCTGGATGGGTGAATCTTCAACAAAGAAATATGCCATCTTGTATCTC 481
QY	421	aagccagaacaacattatgtgttagacaagaattatccattccacacatcaagctgatt 480
DB	482	AAGCCAGAAAACATTATGTTTGTATACAGAAATATTCCTTCCATCAACATCAAGCTGAT 541
QY	481	gactttgtctggctccagaaatagaagatgaggtgaattgaataatttttgggacg 540
DB	542	GACTTTGTCTGGCTCAGCAATAGAAGATGGAGTTGAATTTAAGATAATTTTGGGACG 601
QY	541	ccggaattgtgtgtccagaattgtgaactacgagccctgggtctgggggctgacatg 600
DB	602	CCGGAATTTGTTGCTCCAGAAATTTGTAATACGAGCCCTGGGTCTGGAGGTGACATG 661
QY	601	tggagcataggcgtcatcacctcatctcttaagttagtgagcatccctttctctgggagac 660
DB	662	TGGAGCATAGGCGTCAATACCTACATCTCTTAAAGTGGAGCATCCCTTCTCTGGGAGAC 721
QY	661	acgaagcagggagacactggcaaatatcatcatcagtgagttacgactttgatgaggaattc 720

Db	722	ACGAACGAGAAACACTGGCAATATCATCATGAGTTACGACTTGTATGAGGAATTC 781
QY	721	ttcagccatacagcagcagctggccaaggaacttattcggaagctcttggttaagagacc 780
Db	782	TTCAGCCATACGAGCGAGCTGGCCAAAGGACTTTATTCGGAAGCTTCTGTTAAAGAGACC 841
QY	781	cggaaacgctcacaatccaagaagccttcagacaccccttgatgataccgctggtagaac 840
Db	842	CGGAACCGGCTCAATCCAAAGAGGCTCTCAGACACCCCTGGATCACCGCGGTGGACAAC 901
QY	841	cagcaagccatgggtgcgaaggggagctgtggtcaatcttgagaacttcagaagcagtat 900
Db	902	CAGCAAGCCATGCTGCGCAGGAGTCTGTGGTCAATCTCGAAGCTTCAGGAAGCAGTAT 961
QY	901	gtccgcagggcgtggaagcttcttcagcatcgttcccttgcaacacacacacacacccgc 960
Db	962	GTCCGACGGCGGTGGAAGCTTCTTCAGCATCGTCTCCCTGTGCAACCACTCACCCGC 1021
QY	961	tcgctgatgaagaaggtgcacctgagcggcgatgaggaactgaggaactgtgagagtgc 1020
Db	1022	TCGCTGATGAAGAGGTGCACCTGAGCGCGATGAGGACCTGAGAACTGTGAGAGTGAC 1081
QY	1021	actgagggagacatcgccagaggaagaaagccctccaccacggaggaggagcagcaactcc 1080
Db	1082	ACTGAGGAGGACATGCCAGGAGGAAAGCCCTCCACCCACGAGGAGGAGCAGCACCTCC 1141
RESULT 2		
AB018001	1739 bp	mRNA linear PRI 04-DEC-1999
LOCUS	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds.	
DEFINITION	AB018001.1 GI:6521209	
ACCESSION	Death-associated protein kinase 2.	
VERSION	Homo sapiens cDNA to mRNA.	
KEYWORDS	Homo sapiens	
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
ORGANISM	1 (sites) Nomura, F., Hoshino, K., Copeland, N.G., Gilbert, D.J., Kawai, T., and Akira, S.	
REFERENCE	Jenkins, N.A. and Akira, S. Death-associated protein kinase 2 is a new	
AUTHORS	calcium/calmodulin-dependent protein kinase that signals apoptosis through its catalytic activity	
TITLE	Oncogene 18 (23), 3471-3480 (1999)	
JOURNAL	99303018	
MEDLINE	2 (bases 1 to 1739)	
REFERENCE	Akira, S. and Kawai, T.	
AUTHORS	Direct Submission	
TITLE	Submitted (28-SEP-1998) Shizuo Akira, Hyogo College of Medicine,	
JOURNAL	Department of Biochemistry; Mukogawa-cho 1-1, Nishinomiya, Hyogo	
	663-8501, Japan (E-mail: akira@hyo-med.ac.jp, Tel:81-798-45-6357,	
	Fax:81-798-46-3164)	
FEATURES		Location/Qualifiers
source	1..1739	/organism="Homo sapiens"
	/db_xref="taxon:9606"	
	31..1143	
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gene	31..1143	/gene="DAPK2"
	/codon_start=1	
	/product="Death-associated protein kinase 2"	
	/protein_id="BAA88063.1"	
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	/translation="MFQASMRSPNMEPFKQKVEDFYDIGELSGGQFAIVKKCREKS	
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	LELVSGGELFLAQKESLESEATSFQKLDGVNLYHTKKIAHFDLKPENIMLLDK	
	NIPPIHKLIDFLGAHEIDEGVEFNIFGFEVAPELVIVNIEPLGLEADMWSIGVTY	
	ILLSGASPLGDTKQETLANITSYDFDEEFFSHSELAKDFIRKLLKYEKRRLTI	
	QALRHPIWITPVDNQAMVRESVNVLENFRKQYVRRRWKLSFISVLSLNLHRLSLMK	
	QALRHPIWITPVDNQAMVRESVNVLENFRKQYVRRRWKLSFISVLSLNLHRLSLMK	

Db	961	GTCCGAGCGGGTGGGAAGCTTTCCTTCACATCGTGTCTCCTGTGCAACCACTCACCCGC	1020
QY	961	tcgctgatgaagaagtgccacctgagccggtgaggaagcctgaggaactgtgagagtgcac	1020
Db	1021	TCGCTGATGAAGAAGTGCACCTGAGCGCGGATGAGGACCTGAGGAACCTGTGAGAGTGAC	1080
QY	1021	actgagagagacatcccgaggaggaagcctcccccacgagagagagagagacacccccc	1080
Db	1081	ACTGAGGAGACATCCCGAGGAGGAAGCCCTCCACCCACGAGGAGGAGCAGCACCTCC	1140
RESULT	3		
BC022165			
LOCUS	BC022165	1883 bp	mRNA linear ROD 28-JAN-2002
DEFINITION	Mus musculus, death-associated kinase 2, clone MGC:13742		
ACCESSION	BC022165		
VERSION	BC022165		
KEYWORDS	BC022165.1	GI:18381096	
SOURCE	MGC.		
ORGANISM	house mouse.		
REFERENCE	Mus musculus		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
JOURNAL	Strausberg,R.		
REMARK	1 (bases 1 to 1883)		
COMMENT	Direct Submission		
	Submitted (25-JAN-2002) National Institutes of Health, Mammalian		
	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
	NIH-MGC Project URL: http://mgc.nci.nih.gov		
	Contact: MGC help desk		
	Email: cgabbs-remail.nih.gov		
	Tissue Procurement: Gilbert Smith, Ph.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Institute for Systems Biology		
	http://www.systemsbio.org		
	Contact: amadan@systemsbiology.org		
	Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha		
	Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting		
FEATURES	Clone distribution: MGC clone distribution information can be found		
source	through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov		
	Series: IRAK Plate: 18 Row: f Column: 7		
	This clone was selected for full length sequencing because it		
	passed the following selection criteria: matched mRNA gi: 6521216.		
	Location/Qualifiers		
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	/db_xref="LocusID:13143"		
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	/tissue_type="Mammary tumor metastasized to lung. Tumor		
	arose spontaneously from a senescent normal mammary		
	(clonal) outgrowth infected with the virus MMTV."		
	/clone_lib="NCI CGAP_Lu29"		
	/lab_host="DH10B"		
	/note="Vector: pCMV-SPORT6"		
	1. .1203		
	/codon_start=1		
	/product="death-associated kinase 2"		
	/protein_id="AAH22165.1"		
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	LELVSGGELDFLAQKLSSEBESFTKQILDGVNYLTKTKIAFLDLPKINMLLQK		
	NIPPIKILDFGLAHEIDGVEFKNIFGTGFVAFVINYVEPLGLADKMSIGVIT		
	ILLGASPFPGDTKQETLANITAVSYDDEEFQTSLEANDFKILAVKTRRLT		
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ORIGIN			

polya_site

KVHLRPDLNRNCSDTEEDIARRKALHPRRRSSTS"

1739

/note="17 a nucleotides"

BASE COUNT

439 a 439 c 504 g 357 t

ORIGIN

Query Match

99.3%; Score 1072; DB 9; Length 1739;

Best Local Similarity 99.5%; Pred. No. 2.5e-230;

Matches 1075; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	1	atggagccattcaagcagcagaagtgagagaccttttatgacatcgcgagagagcgtgggg	60
Db	61	ATGGAGCCATTCAAGCAGCAGAAGGTGGAGAGCTTTTATGACATCGGAGAGAGCTGGGG	120
QY	61	agtggccagtgtgccatcgtaagaagtcgccgggagaagacgagcgggtcttgatgtaca	120
Db	121	AGTGGCCAGTTGCCATCGTGAAGAAGTCCGGGAGAAGACGACGGGCTTGAGTATGCA	180
QY	121	gccaaattcatcaagaagcggcagagccggggcgagccggcggtgtgagcgggaggag	180
Db	181	GCCAAATTTCATCAAGAAGCGCAGAGCCGGCGAGCGCGCTGTGAGCGGGAGGAG	240
QY	181	atcgaagcggaggtagcattcctcgccgaggtgctgcaccacaatgtcatcagcgtcac	240
Db	241	ATCAGCGGGAGGTGAGCATCTCTCGCGCAGGTGCTGCACCAATGTATCATCGCTGCAC	300
QY	241	gagctctatgagaaccgcagcagcgtggtgacatccttgagctagtgtctggagagag	300
Db	301	GAGCTCTATGAGAACCGCACCGACCGTGGTGTCTATCTCTTGAGTAGTGTCTGGAGGAG	360
QY	301	ctcttcgattctctgcccagaaggagtcactgagtgagagagccaccagcttcatt	360
Db	361	CTCTTCGATTTCCTGCGCCAGAGGAGTCACTGAGTGAGGAGAGCCACACAGCTTCATT	420
QY	361	aagcagatcctgtagtgggtgaactaccttcacacaaaataatttctcactttgatctc	420
Db	421	AAGCATCTCTGGATGGGTGGAATACCTTTCACACAAAGAAATTTCTCACTTTGATCTC	480
QY	421	aagccagaaaacattatgttgttagacaagaatatctccattccacacatcaagctgatt	480
Db	481	AAGCCAGAAAACATTATGTGTTAGACAGAATATTTCCCATTCACACATCAAGCTGATT	540
QY	481	gacttggctggtgtcacgaaatagaaatggagtgagttgaatttaagaatatattttggagc	540
Db	541	GACTTTGGTCTGGCTCAGCAATAGAAATGGAGTTGAATTTAAGAATATTTTGGGACG	600
QY	541	ccggaatttgttctccagaaaattgtgaactaacgagccctggggtctggaagctgacatg	600
Db	601	CCGGAATTTGTCTCCAGAAATTTGTAACACAGACCCCTGGGTCTGGAGGCTGACATG	660
QY	601	tggagcataggcgtcatcactacatctctttaaagtgagcatccctcttcctgggagac	660
Db	661	TGAGCATAGGCGTCATCATTCTTAAAGTGAGCATCCCTTCCTTGGGAGAC	720
QY	661	acgaagcaggaacactggcaaatatcacatcagtgagtgacttgatgaggaattc	720
Db	721	ACGAAGCAGGAACACTGGCAAAATATCACAGCAGTGAGTTACGACTTTGATGAGGAATTC	780
QY	721	ttcagccatcagcagcagctggccaaaggacctttattcgaagcttctggttaaagagacc	780
Db	781	TTCAGCCAGACGAGCGAGCTGGCCAAAGGACTTTATTTCGGAAGCTTCTGGTTAAAGAGACC	840
QY	781	cggaaagcgtccaatccaagagctcttcagacacccctggatcacgcccgtggacaac	840
Db	841	CGGAACGGCTCATATCCAGAGGCTCTCAGACACCCCTGGATACAGCCCGTGGACAAC	900
QY	841	cagcaagccatggtgcagcgggagtgctgtggtcaactctggagaacttcaggaagcagtat	900
Db	901	CAGCAAGCCATGTCGCAGGGAGTCTGTGTTCAATCTGGAGAACTTCAGGAAGCAGTAT	960
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Db	961	GTCCGCAGCGGTGAAGCTTTCTTCAGCATGCTGTCTCCCTGTGCAACCAACCTCACCCGC	1020
QY	961	tcgctgatgaagaaggtgcacctgagccgagtcgagcctgaggaactgtgagagtgc	1020
Db	1021	TCGCTGATGAAGAAGGTGCACCTGAGCCGGATGAGGACCTGAGGAACCTGTGAGAGTGAC	1080
QY	1021	actgagagagacatcgccagaggaagaagccctccaccacgagagagagagcagcacctcc	1080
Db	1081	ACTGAGGAGGACATCGCCAGGAGGAAGCCCTCCACCCAGGAGGAGGAGCAGCACCTCC	1140
RESULT 3			
LOCUS	BC022165	1883 bp	mRNA linear ROD 28-JAN-2002
DEFINITION	Mus musculus, death-associated kinase 2, clone MGC:13742		
ACCESSION	BC022165	IMAGE:4016911, mRNA, complete cds.	
VERSION	BC022165.1	GI:18381096	
KEYWORDS	MGC.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 1883)		
JOURNAL	Strausberg,R.		
REMARK	Submitted (25-JAN-2002) National Institutes of Health, Mammalian		
COMMENT	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
	NIH-MGC Project URL: http://mgc.nci.nih.gov		
	Contact: MGC help desk		
	Email: cgabps-remail.nih.gov		
	Tissue Procurement: Gilbert Smith, Ph.D.		
	CDNA Library Preparation: Life Technologies, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Institute for Systems Biology		
	http://www.systemsbio.org		
	Contact: amadan@systemsbiology.org		
	Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha		
	Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting		
Clone distribution: MGC clone distribution information can be found			
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov			
Series: IRAC Plate: 18 Row: f Column: 7			
This clone was selected for full length sequencing because it			
passed the following selection criteria: matched mRNA gi: 6521216.			
FEATURES	Location/Qualifiers		
	1..1883		
	/organism="Mus musculus"		
	/db_xref="LocusID:13143"		
	/db_xref="taxon:10090"		
	/clone="MGC:13742 IMAGE:4016911"		
	/tissue_type="Mammary tumor metastasized to lung. Tumor		
	arose spontaneously from a senescent normal mammary		
	(clonal) outgrowth infected with the virus MMTV."		
	/clone_lib="NCI_CGAP_Lu29"		
CDS	/lab_host="DH10B"		
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	91..1203		
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BASE COUNT	576 a 444 c 471 g 392 t		
ORIGIN			

Qy 181 atcagcggagggtgagcattcctgcggcaggtgctgcaccacaatgtcaccagtgcac 240
Db 322 ATCAGCGGGAGGTGAGCATCTCTCGCAGGTGCTGCACCCACATCATCACGCTGCAG 381
Qy 241 gacgtctatgagaaccacacagcagtggtgcacatccttgagctagtgtctggaggagag 300
Db 382 GACGTCTATGAGAACCCACCGAGCTGCTCATCTCTGAGCTAGTGTCCGGAGAGAA 441
Qy 301 ctcttcgatttcttcggccagaaagagtcagtgcagtgagagagccacagcttcatt 360
Db 442 CTGTTTGTATTCCTGGCCCGCAGAGAGTGTAACTGAGGAGGAGGCCACGACTTCATT 501
Qy 361 aagcagatccttggtgggtgaaactccttcacacaagaaaaattgtcactttgatctc 420
Db 502 AAGCAGATCTCTGGATGGGTGAATTACCTTCACACAAGAAAAATTGCTCACTTTGATCTC 561
Qy 421 aagccagaaaaacattatgttttagacaagaataattccattccacacatcaagtatt 480
Db 562 AAGCCAGAAAACATCATGTTGTTAGACAAGAAATATCCCAATTAAACATTTTGGGACA 621
Qy 481 gactttggtctgcgcacgaataagaatgaggtgagttgaatttaagaataatttttgggacg 540
Db 622 GACTTTGGCCTGGCTCAGAAATAGAGATGGAGTTCAATTTAAACATTTTGGGACA 681
Qy 541 ccggaatttgcctcagaaaaattgtgaactacagagccctgggtgctcgtggagctgcacatg 600
Db 682 CCTGAATTTGCTGCTCCAGAAATCGTGAACATATGAGCCACTGGGACTGGAGCCGACATG 741
Qy 601 tggagcattagcgtcatcactacatcctcttaagtggagcatcccttctctgggagac 660
Db 742 TGGAGCATTTGAGTTCATCACCCTATATCTTCTAAAGTGGAGGCTCCCTCTGGGAGAC 801
Qy 661 acgaagcaggaacacactggcaaatatcacatcagtgagttacgactttgatgaggaattc 720
Db 802 ACAAACAAGAAACCTTGGCAAAATATCATGCTGTGAGTTACGACTTTGATGAGGAATTC 861
Qy 721 ttacgccatacagcagcagctggccaaaggactttattcggaaagcttctggttaaagacc 780
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Qy 841 cagcaacgcatgtgcagcggagctgtgtgtaactctgagaacttcaggaagcagtat 900
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RESULT 5
AF052942 1474 bp mRNA linear ROD 20-JAN-2000
LOCUS Mus musculus DAP-kinase related protein 1 mRNA, partial cds.
DEFINITION AF052942
ACCESSION AF052942
VERSION AF052942.1 GI:3560544
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1474)
AUTHORS Inbal,B., Shani,G., Cohen,O., Kissil,J.L. and Kimchi,A.
TITLE Death-associated protein kinase-related protein 1, a novel Serine/threonine kinase involved in apoptosis
JOURNAL Mol. Cell. Biol. 20 (3), 1044-1054 (2000)
MEDLINE 20094983
PUBMED 10629061
REFERENCE 2 (bases 1 to 1474)
AUTHORS Kimchi,A. and Inbal,B.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-1998) Molecular Genetics, Weizmann Institute of Science, Rehovot 76100, Israel
FEATURES
source 1..1474
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/db_xref="taxon:10090"
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BASE COUNT 399 a 356 c 371 g 348 t
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Query Match 72.1%; Score 778.2; DB 10; Length 1474;
Best Local Similarity 90.9%; Pred. No. 2.3e-164;
Matches 828; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 170 gccggggaggagatcagcgggaggtgagcatcctcgcggcaggtgctgcaccacaatgtca 229
Db 1 GCCGGGAGGAAATCGAGCGGAGGTGAGCATCTCTCGCGCAGGTGCTGCACCCACATCA 60

Qy 230 tcacgctgcacgacgctctatgagaacgcgacgcgctggtgcacatccttgagctagtg 289
Db 61 TCACGAGGACGACGAGCTCTATGAGAACCCGACCGAGCTGCTCATCTCTGAGCTAGTGT 120

Qy 290 ctgagagagacgtcttgattctcctgcgcagaaagagtcactgagtgagagagccca 349
Db 121 CCGAGGAGAGAACTGTTTGATTTCCTGCCCCAAGAGGAGTCCTTAAAGTGAGGAGGAAGCCA 180

Qy 350 ccagcttcattaaagcagatccttggtgggtgaaactaccttcacacaaagaaaattgctc 409
Db 181 CCAGCTTCATTAAAGCAGATCTCTGGATGGGTGAATTACCTTCACACAAAGAAATTCGTC 240

Qy 410 acttgatctcaagccagaaaaacattatgttggtagacaagaataattccccattccacaca 469
Db 241 ACTTTGATCTCAAGCCAGAAAAACATCATGTTGTTAGACAAGAAATGCCAATTCACACACA 300

Qy 470 tcaagctgattgactttggtctggtcgcagaaatagaagatggagttgaatttaagaata 529
Db 301 TCAAGCTGATTGACTTTGGCCCTCGGAAATAGAGATGGAGTTCGAATTTAAAAACA 360

Qy 530 ttttgggagcccggaatttgtgtccagaaaattgtgaactacgagccctggggtctgg 589
Db 361 TTTTGGGACACCTGGAATTTGTTCTCCAGAAATCGTGAACTATGAGCCACTGGGACTGG 420

Qy 590 aggtgcacatgtgagcatagcgctcatcacctacatcctcttaagtgagagcaccctt 649
Db 421 AGGCCGACATGTGGAGCATTTGGAGTCATCACTATATCTTCTTAAGTGGAGCGTCCCCCT 480

Qy 650 tcctgggagacacgaagcaggaaaaacactggcaaatatcatcatcagtgaggttacgacttg 709
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Sat May 18 15:09:02 2002

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RESULT 8
AB007144 2105 bp mRNA linear PRI 25-FEB-1998
LOCUS Homo sapiens mRNA for ZIP-kinase, complete cds.
DEFINITION AB007144
ACCESSION AB007144
VERSION AB007144.1 GI:2911155
KEYWORDS ZIP-kinase.
SOURCE .Homo sapiens cDNA to mRNA.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2105)
Akira,S. and Kawai,T.
Direct Submission
Submitted (10-SEP-1997) Shizuoka Akira, Hyogo College of Medicine,
Department of Biochemistry, Mukogawa-cho 1-1, Nishinomiya, Hyogo
663, Japan (E-mail:akira@hyo-med.ac.jp, Tel:+81-798-45-6357,
Fax:+81-798-46-3164)
2 (sites)
Kawai,T., Matsumoto,M., Takeda,K., Sanjo,H. and Akira,S.
ZIP kinase, a novel serine/threonine kinase which mediates
apoptosis
Mol. Cell. Biol. 18 (3), 1642-1651 (1998)
98147805
Location/Qualifiers
1. .2105
/organism="Homo sapiens"
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BASE COUNT 402 a 630 c 741 g 332 t
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Best Local Similarity 76.1%; Pred. No. 3.6e-105;
Matches 634; Conservative 0; Mismatches 199; Indels 0; Gaps 0;
QY 1 atggagccattcaagcagcagaggtgagagcttttatgacatcgagagagctgggg 60
DB 94 ATGTCCACGTTTCAGCAGGAGGAGCGTGGAGGACCATTTATGAGTGGGGAGAGCTGGGC 153
QY 61 agtgccagtttgcattcgtgaagaagtgcgggagagcagcagcgtgtgagccggagag 120
DB 154 AGCGGCCAGTTTGCATCGTCGGAAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAG 213
QY 121 gccaagtttcaagaagcagcagagcagcagcagcagcagcagcagcagcagcagcag 180
DB 214 GCCAAGTTTCATCAAGAAGCGCGCTGTTCATCCAGCGCGGCTGGGTGAGCCGGAGGAG 273
QY 181 atcagcgggaggtgagcattctgcgcagcagcagcagcagcagcagcagcagcagcag 240
DB 274 ATCGAGCGGAGGTGAACATCTCTGGGAGATCCGGACCCCAACATCATCACCTGCAC 333
QY 241 gacgtctatgagaacccagcagcagcagcagcagcagcagcagcagcagcagcagcag 300
DB 334 GACATCTTCAGAACAAAGACGAGCGTGGTCTCATCCCTGGAGCTGCTCTTGGCGGGGAG 393
QY 301 ctcttcgatttctgcccccaagagagtcactgagtgagagagggccaccagcttcatt 360

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DB 394 CTCTTTGACTTCTTGGCGGAGAAAGAGTCGTCGACGGAGGACGAGCCACCGTCTCTC 453
QY 361 aagcagatcctggtggtggaactacccttcacacaaagaaaaatgctcactttgatctc 420
DB 454 AAGCAGATCCTGGACGCGTTCACCTACCTGCACTCTTAAGCGCATCGCACACTTTGACCTG 513
QY 421 aagccgaaaaaacattatgtttagaacaagaatattccattccacacacacacacacacac 480
DB 514 AAGCGGAAAAACATCATCTGCTGGACAGAGTGTGCGGCGCTGGAGCGGAGTACATCAAGTCATC 573
QY 481 gactttggtctggtcaccgaaatagagatgagagtgagagtgagagtgagagtgagagtgag 540
DB 574 GACTTCGCGCATCGCGCAACAAGATCGAGCGGGGGAAGAGTTCAAGAACATCTTCGCGCAC 633
QY 541 ccggaattgtgtccagaaattgaaatcacgagccctgggtctggtggtggtggtggtggtggtg 600
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QY 601 tggagcatagcgctcaccctacatcctcttaagtggagacaccccttccctgggagac 660
DB 694 TGGAGCATCGGTGCATCACCCTATATCTCTGAGCGGTGCATCCCGTTCCTGGCGGAG 753
QY 661 acgaagcaggaacacatggtgaaatcacatcagtgagtgagtgagtgagtgagtgagtgag 720
DB 754 ACCAAGCAGGAGGAGCGCTCACCACATCTCAGCGTGAACACGACTTCGAGCAGGAGTAC 813
QY 721 ttacgcatcacgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 780
DB 814 TTCAGCAACACCAGGAGGAGTGGCCAAAGACTTTCATTCGCGCGCTGCTCTCAAGATCCC 873
QY 781 cggaaacggctcacaatccaagagcgtctcagacacaccccttgatcaccccggt 833
DB 874 AAGCGGAGAAATGACCATTCGCCAGAGCGCTGGAACATCTCTGGATTAAAGCGCAT 926

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RESULT 9
LOCUS AR076189 2132 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 3 from patent US 5958748.
ACCESSION AR076189
VERSION AR076189.1 GI:10002935
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2132)
AUTHORS Akira,S. and Kawai,T.
TITLE DNA coding for serine/threonine kinase
JOURNAL Patent: US 5958748-A 3 28-SEP-1999;
FEATURES
1. .2132
Location/Qualifiers
Source
BASE COUNT 429 a 630 c 741 g 332 t
ORIGIN
Query Match 47.6%; Score 514.6; DB 6; Length 2132;
Best Local Similarity 76.1%; Pred. No. 3.6e-105;
Matches 634; Conservative 0; Mismatches 199; Indels 0; Gaps 0;
QY 1 atggagccattcaagcagcagaggtgagagcttttatgacatcgagagagcagcagcagcagcag 60
DB 94 ATGTCCACGTTTTCAGCAGGAGGAGCGTGGAGGACCATTTATGAGTGGGGAGAGCTGGGC 153
QY 61 agtgccagtttgcattcgtgaagaagtgcgggagagcagcagcagcagcagcagcagcagcag 120
DB 154 AGCGGCCAGTTTGCATCGTCGGAAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 213
QY 121 gccaagtttcaagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 180
DB 214 GCCAAGTTTCATCAAGAAGCGCGCTGTTCATCCAGCGCGGCTGGGTGAGCCGGAGGAG 273

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Best Local Similarity	76.1%;	Pred. No. 3.6e-105;		
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Db	94	ATGTCACGTTTCAGGCAGGAGCAGCTGGAGACCATATATGAGTGGGGAGGAGCTGGGC	153	

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DEFINITION	E23384	linear
ACCESSION	E23384	
VERSION	E23384.1	
KEYWORDS	JP 1999098984-A/1.	
SOURCE	unidentified.	
ORGANISM	unidentified.	
REFERENCE	1 (bases 1 to 2132)	

SOURCE	ORGANISM
unidentified.	
unidentified	
unclassified.	
unclassified.	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 2132) Shizuo, S. T. K. K.	DNA encoding serine/threonine kinase Patent: JP 199098984-A 1 13-APR-1999;	SCIENCE & TECH AGENCY	
	OS	Unidentified		
	PN	JP 199098984-A/1		
	PD	13-APR-1999		
	PF	26-SEP-1997	JP 1997261589	

PR	SHIZUO SHINRA-TARO KAWAI
PI	C12N15/09,C12N1/21,C12N9/12//C12N15/09,C12R1:91),(C12N1/21,
PC	C12N15/09,C12N1/21,C12N9/12),C12N15/00,C12R1:91) CC
PC	C12R1:19),
PC	(C12N9/12,C12R1:19),C12N15/00,C12N15/00,C12R1:91) CC
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CC	Topology: Linear;
FH	Key
FT	CDS
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Best Local Similarity	76.1%; Pred. NO.3.6e-105;
Matches 634; Conservative	0; Mismatches 199; Indels 0; Gaps 0;
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QY	94 ATGTCACGTTTCAGCAGCAGGAGCTGGAGGACCATTATCAGATGGGGAGGAGCTGGGC 153
Db	
QY	61 agtggccagtttgccttcgtgaagaagtccgggagagaagacagcggtcttaagtatgca 120
Db	
QY	154 AGCGGCCAGTTTGCATCGTTCGGAAGTTCGCGGAGAACGGCAGCGGCAAGGACTACGCA 213
Db	
QY	121 gccaaattcatcaagaagcgcagagccggcgagccgcgcgtgtgagccgggagaggag 180
Db	
QY	214 GCCAAGTTTCATCAAGAAGCGCGCCTGTCTATCCAGCGCGGTGGGTGTAGCCGGGAGGAG 273
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QY	181 atcgagcggaggtgagcatctctgcgcgaggtgctgtgcacacacacatgtcatcagcgtgcac 240
Db	
QY	274 ATCAGCGGAGGTGAACATCTCTGCGGGAGATCCGGCACCCCAACATCATCACCTTCGAC 333
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QY	241 gaagctatgagaacgcagccagcagctggtgacatctcttgagctagtgtctggagagagag 300
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QY	334 GACATCTTCGAGAACCAAGACGACGTGTCTCTCATCTCTGAGCTGGTCTCTGCGGGGAG 393
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QY	301 ctcttcgattcttcgtgccagaagagtgactgtagtggagggaggccaccagcttcatt 360
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QY	394 CTCTTTGACTTCTTGGCGGAGAAAGATGCCTGACGGGAGGACGAGGCCACCACTTCCCTC 453
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QY	361 aagcagatctctgtagtgggtgaaactacctcacaaagaaaattgctcaactttgatctc 420
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QY	421 aagcagaaaaacattatgttttagacaagaataattcccaattccacacatcaagctgatt 480
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QY	694 TGGAGCATCGGTGTATCACCATTATCTCTGAGCGGTGCATCCCGCTTCCTGGCGAG 753
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QY	661 acgaagcaggaacactggcacaatatcacatcagtagtgattacagactttgataggaaattc 720
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QY	754 ACCAAGCAGGAGACGCTCAACAACTCTCAGCCGTGAACCTTACGACTTCACGAGGAGTAC 813
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QY	721 ttcagccatacagagcagctgcccgaagacttatttcggaagcttctgtgttaaaagacc 780
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QY	814 TTCAGCAACACACAGGAGCTGCCAAGGACTTCATTCCCGCGGTGCTCGTCAAGATGCC 873
Db	

Db	455	GACATCTTCGAGAACAGACGGACGTGGTCTCATCTCGAGTGTCTCTGGCGGGAG	514
Qy	301	ctcttcgattctctggccagaaagagtcactgagtgagagagccaccagcttcatt	360
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Qy	361	aagcagatcctcggatggggtggaactaccttcacacaaagaaaaattgctcactttgatctc	420
Db	575	AAGCAGATCTCTGGACGGCTTCACTACCTGCACTCTAAGCGCATCCGACACATTTGACCTG	634
Qy	421	aagccagaaaaacattatgtttagacagaagaattatcccatccacacatcaagctgatt	480
Db	635	AAGCCGGAAAAACATCATGTCTGTGGACAAAGACGTGCCAACCCAGCAATCAAGCTCATC	694
Qy	481	gactttggtctggtcctcacgaaatagagatggagttgaattttaagaatatattttggagcg	540
Db	695	GACTTCGCATTCGGCGACAGATCGAGGGGGGAAGAGTTCGAAGAACATCTTCGGCACCC	754
Qy	541	ccggaatttgtgtccacgaattgtgaactacagagccctgggtctggaggtgacatg	600
Db	755	CCGGAGTTTGTGGCCCCCAGAGATTGTGAATATGAGCCGCTGGGCTGGAGGCGGACATG	814
Qy	601	tggagcataggcgctacatccatcacatccctttaagtggagcatcccttctcctggagac	660
Db	815	TGGAGCATCGGTGTCTACCTATATCTCTGAGCGGTGCATCCCGCTTCTTGGCGGAG	874
Qy	661	acgaagcagggaaacactggtcgaatatacacatcagtgagttacagctttgatgaggaattc	720
Db	875	ACCANGCAGGAGAGCGTCCACCAACATCTCAGCCGTGAACCTTCGAGTTCGAGGAGGATAC	934
Qy	721	ttcagccatcacgagcagctggccaaagactttatttcggaagcttcttggttaagagacc	780
Db	935	TTCAGCAACACGGCGGAGCTGGCCAAAGACTTCAATTCGCCGGCTGCTCGTCAAGATCCC	994
Qy	781	cggaaacggtctcaaatccaaagaggtctcagacacccccctggatcacgcccgt	833
Db	995	AAGCGGAGAATGACCATTCGCCAGAGCGCTGGAACATCTCTCGATTAAAGCGCAT	1047
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AK027590			
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DEFINITION	AK027590		
ACCESSION	AK027590.1 GI:14042369		
VERSION	Homo sapiens teratocarcinoma cell_line:NT2 cDNA to mRNA,		
KEYWORDS	oligo capping; fis (full insert sequence).		
SOURCE	clone_lib:NT2RP2 clone:NT2RP2004933.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (sites)		
Isogai,T., Ota,T., Hayaishi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sudano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A.			
NEDO human cDNA sequencing project			
Unpublished			
JOURNAL	2 (bases 1 to 2224)		
REFERENCE	Isogai,T. and Otsuki,T.		
AUTHORS	Direct Submission		
TITLE	Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan		
JOURNAL	(E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,		
COMMENT			

University of Tokyo.	
FEATURES	Location/Qualifiers
source	1..2224
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BASE COUNT	419 a 656 c 806 g 343 t
ORIGIN	
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Matches 634; Conservative 0; Mismatches 199; Indels 0; Gaps 0;	
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Db	215 ATGTCACGTTTACGAGCAGGAGACGTGGAGACCATTTATGAGATGGGGAGGAGCTGGC 274
QY	61 agtgccagtttgccatcgtgaagaagtcgcccgggagaagagcacggggttgagatgca 120
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QY	121 gccaaagttaacaagaagcggcagagccggcgagcggcggtgtgagccgggagag 180
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Db	455 GACATCTTCGAGAACAGACGGACGTGCTCTCATCTCGAGGCTGGTCTCTGGCGGGAG 514
QY	301 ctcttgcattctggtcccaagaaggagtcactgagtgagagagggccacagcttcatt 360
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Db	635 AAGCCGGAANAACATCATGTCTGTGGACAAAGACGTGCCAACCCACGAAATCAAGCTCATC 694
QY	481 gactttggtctggtccagaaatagagatgagttgaatttaagaatttttggagag 540
Db	695 GACTTCGGCATCGCGCACAAAGATCGAGCGGGGAACGAGTTTCAAGAACATCTTCGGCACCC 754
QY	541 ccggaatttgtgtccagaaattgtgaactacagcccttgggtcttgagagctgacatg 600
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QY	601 tggagcataggcgctacacctacatccctttaaagtggagcatcccttctcctgggagac 660
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QY	661 acgaagcaggaacaaactggtcgaatatacacatcagtgagttacgacttttgatgagaattc 720
Db	875 ACCAAGCAGGAGACGCTTCACCAACATCTCAGCCGTGAACCTTCGAGGAGGAGTAC 934
QY	721 ttacgccatcacgagcagctggccaaagactttatttcggaagcttcttggttaagagacc 780
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QY	781 cggaaacggtctacaaatccaaagaggtctctcagacacccccctggatcacgcccgt 833

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RESULT	15
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ACCESSION	AR076190
VERSION	AR076190.1 GI:10002936
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SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 1429).
AUTHORS	Akira,S. and Kawai,T.
TITLE	DNA coding for Serine/threonine kinase
JOURNAL	Patent: US 5958748-A 4 28-SEP-1999;
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QY	61	a g t g g c c a g t t t g c c a t c g t g a a g a a g t c c g g g a g a a g a c a c g g g g c t t g a g t a t g c a	120		
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QY	121	g c c a a g t t c a t c a a g a a g c g g a g a c c g g g c g a g c c g c g c g t g t g a c c c g g g a g g a y	180		

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DEFINITION Mus musculus mRNA for ZIP-kinase, complete cds.
ACCESSION AB007143
VERSION    AB007143.1 GI:2911153
KEYWORDS   ZIP-kinase.
SOURCE     Mus musculus CDNA to mRNA.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE AUTHORS           Kawai,T., Matsumoto,M., Takeda,K., Sanjo,H. and Akira,S.
TITLE      Submitted (10-SEP-1997) Shizuo Akira, Hyogo College of Medicine,
JOURNAL    Department of Biochemistry; Mukogawa-cho 1-1, Nishinomiya, Hyogo
MEDLINE    663, Japan (E-mail:akira@hyo-med.ac.jp, Tel:+81-798-45-6357,
FEATURES   Fax:+81-798-46-3164)
            2 (sites)
            Kawai,T., Matsumoto,M., Takeda,K., Sanjo,H. and Akira,S.
AUTHORS     ZIP kinase, a novel serine/threonine kinase which mediates
TITLE       apoptosis
JOURNAL     Mol. Cell. Biol. 18 (3), 1642-1651 (1998)
MEDLINE     98147805
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            FGKQTUTNLSAVNYDPDEFYFSSTLSHKSMPENTSYAFSRFSLVEDVAEAEGQL
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polyA_site 1410
BASE COUNT 290 a 425 c 475 g 220 t
ORIGIN
Query Match 47.5%; Score 512.8; DB 10; Length 1410;
Best Local Similarity 76.2%; Pred. No. 8.8e-105;
Matches 631; Conservative 0; Mismatches 197; Indels 0; Gaps 0;
Qy 1 atggagcattcaacgacgaaggctggagacctttatgacatcgagagagactgggg 60
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